In The Claims:

Please amend claims 1, 41-55 and 83, and add claims 123-138, as indicated below in the associated claim listing provided on separate sheets:

1. (Currently Amended) A process for producing one or more portions of a ~~at least one~~ genome wide map, comprising ~~the steps of~~:

(a) receiving single DNA molecules ~~preparing chromosome~~ maps derived from the DNA of a single individual ~~associated with at least one chromosome~~; and

(b) using a hardware processing arrangement, producing the one or more ~~a~~ portions of the ~~at least one~~ genome wide map based on the single DNA molecules maps ~~chromosome maps~~, wherein the ~~at least one~~ genome wide map comprises at least one of a haplotyped genome wide map or a genotyped genome wide map.

Claims 2-40 (Canceled).

41. (Currently Amended) A non-transitory computer-accessible medium having stored thereon computer executable instructions ~~software arrangement~~ which, when the executable instructions are executed on a processing device, configures the processing device to produce one or more portions of a ~~at least one~~ genome wide map by procedures which comprise ~~the software arrangement comprising~~:

(a) receive single DNA molecules ~~a first set of instructions which are capable of configuring the processing arrangement to prepare chromosome~~ maps derived from the DNA of a single individual ~~associated with at least one chromosome~~; and

(b) ~~a first set of instructions which are capable of configuring the processing arrangement to~~ produce the one or more ~~a~~ portions of the ~~at least one~~ genome wide map based on the single DNA molecules maps ~~chromosome maps~~, wherein the ~~at least one~~ genome wide map comprises at least one of a haplotyped genome wide map or a genotyped genome wide map.

42. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 41, wherein the one or more portions of the ~~at least one~~ genome wide map comprises at least one restriction site.

43. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 41, wherein less than all subparts of the genome wide map are produced in step (b) as ordered or unordered sets of contigs.

44. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 41, wherein the single DNA molecules ~~chromosome~~ maps are based on at least one single molecule map data set.

45. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 41, wherein the genome wide map comprises two maps per autosomal chromosome and is assembled from the at least one single molecule map data set

46. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 44, wherein the at least one single molecule map data set has error rates as great as or smaller than: at least one of (i) about 10% error in distance between sites, (ii) about 20% missing sites, (iii) about 7% false sites ~~and~~ or (iv) about 50% of sites closer than about 1 kB apart that are indistinguishable.

47. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 44, wherein the at least one single molecule map data set ~~consists of~~ comprises at least one of ~~either~~ (i) Optical Mapping data or (ii) any single molecule ordered maps of polymorphic markers comprising at least one of restriction site polymorphisms, restriction length polymorphisms, insertions of bases, deletions of bases, or single nucleotide polymorphisms ~~(SNPs)~~.

48. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 44, wherein the at least one single molecule map data sets comprising different restriction site markers are assembled into a single genome wide map, wherein ~~all~~ the restriction site markers are combined, and wherein the restriction site markers ~~can be~~ are distinguishable~~d~~.

49. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 41, wherein the executable instructions further configure the processing device to ~~further comprising~~ determine~~ing~~ a conditional probability density expression.

50. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 49, wherein the probability density expression is based on errors provided in at least one single molecule map data set.

51. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 41, wherein substantially all site based polymorphisms are detected in the at least one genome wide map.

52. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 41, wherein substantially all interval-based polymorphisms are detected in the at least one genome wide map.

53. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 41, wherein the executable instructions further configure the processing device to perform steps (a) and (b) ~~are performed~~ within a particular time limit, and wherein the particular time is bounded from above by a less than quadratic ~~a sub-quadratic~~ function of a number of sites associated with ~~an~~ input data.

54. (Currently Amended) The computer-accessible medium ~~software arrangement~~ according to claim 41, further comprising performing a disease gene association study based on at least one genome wide map per individual patient.

55. (Currently Amended) A non-transitory computer-accessible medium having stored thereon computer executable instructions ~~software arrangement~~ which, when the

executable instructions are executed on a processing device, configures the processing device to perform procedures ~~disease gene association based on at least one haplotyped genome wide map per patient, the software arrangement~~ comprising:

(a) ~~a first set of instructions which are capable of configuring the processing arrangement to~~ generate a haplotyped genome wide map per each individual one of at least one patient; and

(b) ~~a second set of instructions which are capable of configuring the processing arrangement to~~ perform a ~~the~~ disease gene association based on the ~~produced~~ generated haplotyped genome wide map of each individual one of the at least one patient.

Claims 56-82 (Canceled).

83. (Currently Amended) A system for producing one or more portions of a ~~at least one~~ genome wide map comprising a non-transitory storage medium, wherein the storage medium includes software that is executed by a hardware processing arrangement to perform procedures comprising ~~the steps of~~:

(a) receiving single DNA molecules ~~preparing chromosome~~ maps derived from the DNA of a single individual ~~associated with at least one chromosome~~; and

(b) producing the one or more ~~a~~ portions of the ~~at least one~~ genome wide map based on the single DNA molecules maps ~~chromosome maps~~, wherein the ~~at~~

~~least one~~ genome wide map comprises at least one of a haplotyped genome wide map or a genotyped genome wide map.

Claims 84-122 (Canceled).

123. (New) The process of claim 1, wherein procedures (a) and (b) are performed within a particular time that is bounded from above by a less than quadratic function of a number of sites associated with input data.

124. (New) The process of claim 123, wherein the hardware processing arrangement comprises one or more processors, and procedures (a) and (b) are performed using a single processor.

125. (New) The process of claim 123, wherein procedures (a) and (b) are performed using n^k number of computational steps, where n is a number of sites associated with input data and k is less than 2.

126. (New) The computer-accessible medium according to claim 53, wherein the processing device comprises one or more processors, and wherein procedures (a) and (b) are performed using a single processor.

127. (New) The computer-accessible medium according to claim 53, wherein the processing device is configured to perform procedures (a) and (b) using n^k number of

computational steps, where n is a number of sites associated with input data and k is less than 2.

128. (New) The system according to claim 83, wherein procedures (a) and (b) are performed within a particular time, which is bounded from above by a less than quadratic function of a number of sites associated with input data.

129. (New) The system according to claim 128, further comprising a processing arrangement including one or more processors, and wherein procedures (a) and (b) are performed using a single processor.

130. (New) The system according to claim 128, wherein procedures (a) and (b) are performed using n^k number of computational steps, where n is a number of sites associated with input data and k is less than 2.

131. (New) The computer-accessible medium according to claim 55, wherein the producing procedure comprises the sub sub-procedures of:

(a) receiving single DNA molecules maps derived from the DNA of a single individual; and

(b) producing one or more portions of the genome wide map, wherein the genome wide map comprises at least one of a haplotyped genome wide map or a genotyped genome wide map.

132. (New) The computer-accessible medium according to claim 55, wherein the single DNA molecules maps data set has error rates as great as or smaller than at least one of: (i) about 10% error in distance between sites, (ii) about 20% missing sites, (iii) about 7% false sites, or (iv) about 50% of sites closer than about 1 kB apart that are approximately indistinguishable.

133. (New) A process for performing a disease gene association based on at least one genome wide map, comprising:

producing at least one haplotyped genome wide map for each individual one of at least one patient; and

performing the disease gene association based on the produced at least one haplotyped genome wide map of each individual one of the at least one patient.

134. (New) The process according to claim 133, wherein the producing procedure comprises the sub-procedures of:

(a) receiving single DNA molecules maps derived from the DNA of a single individual; and

(b) producing one or more portions of the at least one genome wide map, wherein the at least one genome wide map comprises at least one of the at least one haplotyped genome wide map or a genotyped genome wide map.

135. (New) The process according to claim 134, wherein the single DNA molecules maps data set has error rates as at most at least one of: (i) about 10% error in distance

between sites, (ii) about 20% missing sites, (iii) about 7% false sites, or (iv) about 50% of sites closer than about 1 kB apart that are approximately indistinguishable.

136. (New) A system for performing a disease gene association based on at least one genome wide map, the system comprising a non-transitory storage medium, wherein the storage medium includes software that is executed by a hardware processing arrangement to perform procedures comprising:

producing at least one haplotyped genome wide map for each individual one of at least one patient; and

performing the disease gene association based on the produced at least one haplotyped genome wide map of each of the at least one individual one of the at least one patient.

137. (New) The system according to claim 136, wherein the producing procedure comprises the sub-procedures of:

(a) receiving single DNA molecules maps derived from the DNA of a single individual; and

(b) producing one or more portions of the at least one genome wide map, wherein the at least one genome wide map comprises at least one of the at least one haplotyped genome wide map or a genotyped genome wide map.

138. (New) The system according to claim 137, wherein the single DNA molecules maps data set has error rates at most at least one of: (i) about 10% error in distance

between sites, (ii) about 20% missing sites, (iii) about 7% false sites, or (iv) about 50% of sites closer than about 1 kB apart that are approximately indistinguishable.